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molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said RNA in said selected organism, and wherein said oligonucleotide does not comprise the iron response element.

A35
--35. An oligonucleotide comprising a molecular interaction site that is present in the RNA of a selected organism and in the RNA of at least one additional organism, wherein said molecular interaction site serves as a binding site for at least one molecule that when bound to said molecular interaction site modulates the expression of said RNA in said selected organism, wherein said oligonucleotide does not comprise the iron response element, wherein said molecular interaction site is identified by a method comprising:

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comparing the nucleotide sequence of said target nucleic acid with the nucleotide sequences of a plurality of nucleic acids from different taxonomic species;

identifying at least one sequence region which is conserved among said plurality of nucleic acids and said target nucleic acid;

determining whether said conserved region has secondary structure; and

for said conserved region having secondary structure, identifying said secondary structure.

36. The oligonucleotide of claim 35 wherein said method further comprises identifying at least one structural motif for said conserved region having secondary structure.

37. The oligonucleotide of claim 36 wherein said method further comprises constructing a set of descriptor elements for said structural motif.

38. The oligonucleotide of claim 37 wherein said method further comprises identifying further nucleic acids having secondary structures corresponding to said descriptor elements.

cell.
39. The oligonucleotide of claim 35 wherein said target nucleic acid is present in a eukaryotic

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40. The oligonucleotide of claim 39 wherein said target nucleic acid is selected from the group consisting of mRNA, pre-mRNA, tRNA, rRNA, and snRNA.

41. The oligonucleotide of claim 35 wherein said target nucleic acid is present in a prokaryotic cell.

42. The oligonucleotide of claim 35 wherein said nucleotide sequence of said target nucleic acid is determined by assembling a plurality of expressed sequence tags.

43. The oligonucleotide of claim 35 further comprising comparing said target nucleic acid to paralogous nucleic acids.

44. The oligonucleotide of claim 35 wherein said plurality of nucleic acids from different taxonomic species is obtained by performing a sequence similarity search, an ortholog search, or a combination thereof.

45. The oligonucleotide of claim 35 wherein said plurality of nucleic acids from different taxonomic species is obtained by performing a sequence similarity search and constructing virtual transcripts.

46. The oligonucleotide of claim 35 wherein determining whether said conserved region has secondary structure is performed by self complementarity comparison, alignment and covariance analysis, secondary structure prediction, or a combination thereof.

47. The oligonucleotide of claim 46, wherein said secondary structure comprises at least one bulge, loop, stem, hairpin, knot, triple interact, cloverleaf, or helix.